ABSTRACT

[0071] Methods are disclosed for predicting family and individual genetic risk of disease through the analysis of very large families (VLFs). A predetermined founder is identified. The definition of family is broadened to include about 100 or more decedents from the founder. The VLF can then be linked to a disease registry to determine if there is a significant excess of disease. This method can further identify individuals at risk for disease. The identified individuals and their immediate family members can then provide DNA samples. These samples can be used to identify the susceptibility gene.

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